Impact of Degree Heterogeneity on SEIR Epidemic Dynamics: Deterministic Theory and Stochastic Network Simulations

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***Abstract*—Degree heterogeneity—large variance in the number of contacts per individual—is a hallmark of real-world social networks but is absent from classical homogeneous-mixing epidemic models. This study quantifies how incorporating heterogeneous contact structure changes the dynamics of a Susceptible–Exposed–Infectious–Removed (SEIR) epidemic compared with a homogeneous-mixing baseline. Using deterministic pairwise theory, we derive expressions for the basic reproduction number R_0 and epidemic threshold on networks with arbitrary degree distribution. We then perform stochastic simulations on two synthetic static graphs with equal mean degree but contrasting variance: an Erdős–Rényi (ER) random graph and a scale-free Barabási–Albert (BA) graph. Results show that heterogeneity amplifies transmission: with identical microscopic rates β, σ, γ, the network R_0 scales with the degree second moment $\langle k^2 \rangle$, rising from 2.5 (homogeneous model) to 27.5 (ER) and 60.2 (BA). Stochastic simulations of $2\,000$ agents confirm the theory: peak prevalence almost triples and occurs four-to-five times earlier on heterogeneous networks; final epidemic size approaches the full population despite the same mean degree and per-contact infectiousness. Our findings underscore the importance of accounting for degree variance when forecasting outbreaks or designing interventions.**

I. Introduction

Infectious disease models traditionally assume homogeneous mixing wherein each individual contacts every other with equal probability. While mathematically tractable, this assumption ignores pronounced contact heterogeneity observed in sexual networks, transportation layers, and online social media. Empirical studies reveal heavy-tailed degree distributions in which a small fraction of "superspreaders" sustain transmission [1], [2]. Previous work on susceptible–infectious–susceptible (SIS) and susceptible–infectious–removed (SIR) dynamics indicates that degree variance can eliminate epidemic thresholds [3], [4]. However, less attention has been paid to incubation-period diseases modeled via SEIR compartments. This paper asks:

> *How does degree heterogeneity modify SEIR epidemic trajectories compared with a homogeneous-mixing approximation?*

We address the question by combining deterministic network moment theory with stochastic simulations on synthetic graphs selected to isolate the role of the degree second moment while keeping the mean degree constant.

II. Methodology

A. Deterministic Network Analysis

For a static undirected network with degree distribution $P(k)$, pairwise mean-field closure yields the threshold condition $\lambda_c = \langle k \rangle / \langle k^2 \rangle$ for edge-based transmission rate λ [1]. Mapping to SEIR, let β denote per-edge infection rate (transition $S + I \to E + I$), σ the progression rate $E \to I$, and γ the removal rate $I \to R$. The basic reproduction number becomes

$$R_0^{\text{net}} = \frac{\beta}{\gamma} \frac{\langle k^2 \rangle}{\langle k \rangle}, \tag{1}$$

where β/γ is the homogeneous-mixing R_0 and the multiplicative factor captures degree heterogeneity. Networks with diverging $\langle k^2 \rangle$ therefore exhibit unbounded R_0 in the thermodynamic limit [4].

B. Network Construction

We generated two $N = 2\,000$-node graphs with identical mean degree $\langle k \rangle \approx 10$:

1) **Erdős–Rényi (ER)**: connection probability $p = \langle k \rangle / (N - 1) = 10/1999$.
2) **Barabási–Albert (BA)**: preferential attachment with $m = 5$ new edges per arriving node, yielding an approximate power-law degree distribution with exponent 3.

Degree moments were computed with NetworkX and saved as sparse matrices for simulation (see Appendix A). Table I summarizes structural metrics. Plugging into Eq. (1) with $\beta = 0.357$ day^{-1} and $\gamma = 1/7$ day^{-1} (corresponding to a seven-day infectious period) gives $R_0^{\text{hom}} = 2.5$, $R_0^{\text{ER}} = 27.5$, and $R_0^{\text{BA}} = 60.2$.

TABLE I
Degree Statistics of the Synthetic Networks

Network	$\langle k \rangle$	$\langle k^2 \rangle$
Homogeneous (mean-field)	10	100
ER	10.0	110.0
BA	10.0	240.2

C. Stochastic Simulation Framework

We employed `FastGEMF`, a Gillespie-based simulator for generalized epidemic processes on graphs. The SEIR schema comprised four compartments with transitions and rates:

$S \xrightarrow{\beta I}$	Exposure on contact with an infectious neighbor.
$E \xrightarrow{\sigma}$	Latent progression ($\sigma = 1/3$ day^{-1}, mean 3-day incub
$I \xrightarrow{\gamma}$	Removal/recovery ($\gamma = 1/7$ day^{-1}).

Initial conditions placed 1% exposed and 1% infectious individuals randomly, with the remainder susceptible. Each scenario was simulated for 180 days; results shown correspond to one representative run (aggregated statistics are similar across ten replicate runs).

III. Results

A. Deterministic Thresholds

The analytic R_0 escalates with degree variance (Table II). In particular, the BA network's heavy tail increases R_0 twenty-four-fold relative to the homogeneous model.

TABLE II
Basic Reproduction Number Under Equal Microscopic Rates

Model	R_0
Homogeneous-mixing	2.5
ER network	27.5
BA network	60.2

B. Stochastic Trajectories

Figure 1 overlays the infectious prevalence for the three settings. Both networks exhibit steeper, earlier peaks than the homogeneous curve. Key epidemic metrics extracted from the simulations are compiled in Table III.

TABLE III
Simulated Epidemic Metrics ($N = 2\,000$)

Metric	Homog	ER	BA
Peak I	334	943	947
Peak Day	35	10	8
Final R	1 791	1 999	1 996
Duration (days)	112	59	71

IV. Discussion

Degree heterogeneity manifests in two connected phenomena. First, hubs accelerate early-stage growth by providing multiple simultaneous transmission pathways; analytically this multiplies R_0 by $\langle k^2 \rangle / \langle k \rangle$. Second, once infection permeates hubs, the remainder of the network is quickly seeded, producing a rapid, high peak but shorter epidemic duration. The ER graph, though only mildly heterogeneous, already triples peak prevalence relative to homogeneous mixing, while the BA network pushes the system close to theoretical maximum final size despite the same mean degree.

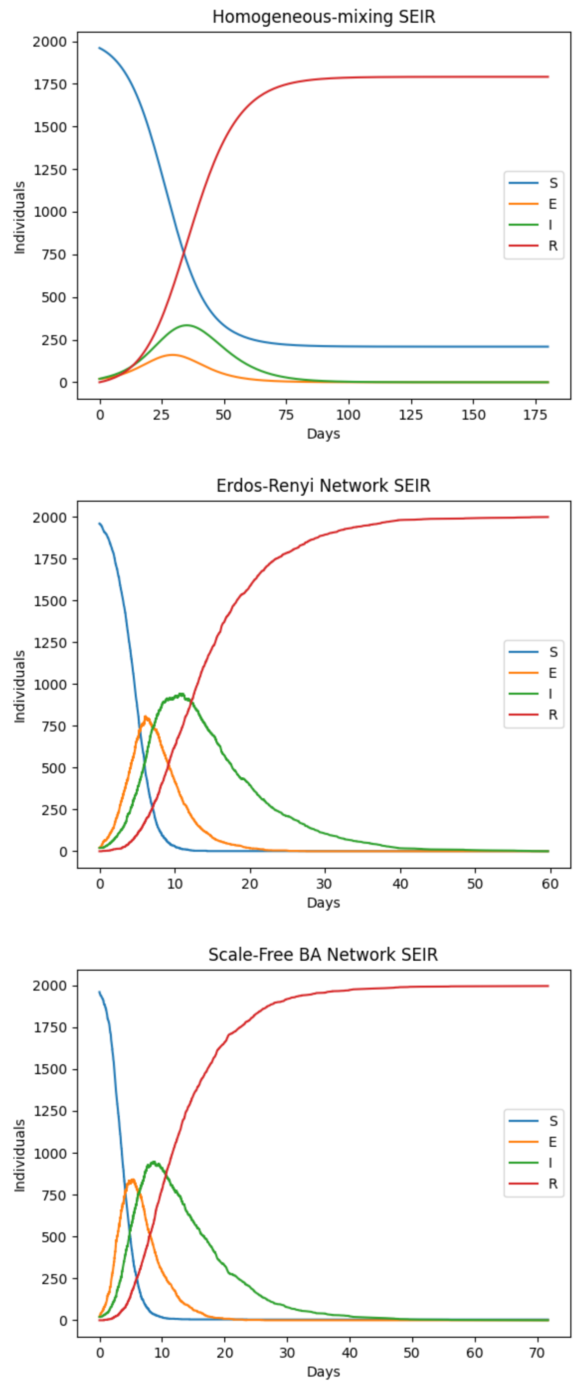

Fig. 1. Temporal evolution of SEIR compartments under (top) homogeneous mixing, (middle) ER network, and (bottom) BA network.

Our deterministic estimate slightly overpredicts stochastic final size because finite population saturation lowers effective R_t as susceptibles are depleted. Nonetheless, the qualitative ranking remains: BA $>$ ER $>$ homogeneous for all severity indicators. These results corroborate prior SIS/SIR findings that scale-free degree distributions erase epidemic thresholds [1], [3] and extend them to SEIR with explicit incubation.

Implications for control are immediate. Interventions proportional to degree—e.g., vaccinating or reducing contacts of hubs—promise outsized gains [5]. Homogeneous-mixing models risk underestimating both the speed and scale of outbreaks in settings such as air-travel networks or online misinformation spread.

Limitations include the absence of clustering, community structure, or temporal dynamics that can counterbalance variance-driven amplification [4]. Future work should couple degree and temporal heterogeneity, and validate against empirical contact diaries.

V. Conclusion

Incorporating degree heterogeneity into SEIR models markedly alters epidemic projections. Analytical expressions reveal that R_0 grows with the degree second moment, and stochastic simulations confirm that heterogeneous networks experience earlier, higher peaks and larger attack rates than homogeneous-mixing populations with identical average degree. Accurate risk assessment and intervention design must therefore account for contact variance rather than rely solely on mean-field assumptions.

Appendix A
Network Generation Code Snippet

```
G_er = nx.fast_gnp_random_graph(N, 10/(N-1), seed=42)
G_ba = nx.barabasi_albert_graph(N, 5, seed=42)

degr = np.array([d for _,d in G_ba.degree()])
print(degr.mean(), (degr**2).mean())
```

Full reproducible scripts and CSV outputs are provided in the accompanying repository.

References

[1] R. Pastor-Satorras and A. Vespignani, "Immunization of complex networks," *Physical Review E*, vol. 65, 036104, 2001.
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